IFWO

RAW SEQUENCE LISTING   DATE: 07/30/2004
PATENT APPLICATION: US/10/796,669A   TIME: 11:26:55

Input Set : **A:\741179.txt**
Output Set: **N:\CRF4\07302004\J796669A.raw**

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 3 <110> APPLICANT: Wang, Jin-Town
 4         Lin, Tzu-Lung
 6 <120> TITLE OF INVENTION: A TYPE II RESTRICTION ENDONUCLEASE AND APPLICATION THEREOF
 8 <130> FILE REFERENCE: P/741-179
10 <140> CURRENT APPLICATION NUMBER: 10/796,669A
11 <141> CURRENT FILING DATE: 2004-03-09
13 <160> NUMBER OF SEQ ID NOS: 5
15 <170> SOFTWARE: PatentIn version 3.2
17 <210> SEQ ID NO: 1
18 <211> LENGTH: 5
19 <212> TYPE: DNA
20 <213> ORGANISM: Helicobacter pylori
22 <400> SEQUENCE: 1
23 ccatc                                                             5
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27 <211> LENGTH: 1617
28 <212> TYPE: DNA
29 <213> ORGANISM: Helicobacter pylori
32 <220> FEATURE:
33 <221> NAME/KEY: CDS
34 <222> LOCATION: (1)..(1617)
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38 Met Thr Lys Lys Pro Ala Arg Lys Ile Leu Ser Phe Ser Thr Thr Met
39 1               5                   10                  15
41 cga aac cct aaa aga ata gga caa ttt tta gct gtt tta gga aag ttt      96
42 Arg Asn Pro Lys Arg Ile Gly Gln Phe Leu Ala Val Leu Gly Lys Phe
43             20                  25                  30
45 gaa aat caa atc ctt aaa tct tca ata atc atg caa att atc aaa tcc     144
46 Glu Asn Gln Ile Leu Lys Ser Ser Ile Ile Met Gln Ile Ile Lys Ser
47         35                  40                  45
49 gtt ttg gct cat agg ctt tat aga cct act tct ctc aat caa aat aaa     192
50 Val Leu Ala His Arg Leu Tyr Arg Pro Thr Ser Leu Asn Gln Asn Lys
51     50                  55                  60
53 gaa ttg aaa gaa aaa ttt gac tcc aat gaa tat gtc ttt agc gat gaa     240
54 Glu Leu Lys Glu Lys Phe Asp Ser Asn Glu Tyr Val Phe Ser Asp Glu
55 65                  70                  75                  80
57 gag tta gaa cgc att ata gaa ata tcc cca caa aat cat aaa gaa atg     288
58 Glu Leu Glu Arg Ile Ile Glu Ile Ser Pro Gln Asn His Lys Glu Met
59             85                  90                  95
61 ggc ttt gag cat gga tgg gaa agc cgg ttt gac act tgg tat aag ctt     336
62 Gly Phe Glu His Gly Trp Glu Ser Arg Phe Asp Thr Trp Tyr Lys Leu
63             100                 105                 110
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65  atg tgt gag ttt ggt ttt tgc tac tat gca aaa tat gag aaa ata ctc         384
66  Met Cys Glu Phe Gly Phe Cys Tyr Tyr Ala Lys Tyr Glu Lys Ile Leu
67          115                 120                 125
69  atc agc gat agc gct aag atg ctt att ctt gct tat tac aat aaa gaa         432
70  Ile Ser Asp Ser Ala Lys Met Leu Ile Leu Ala Tyr Tyr Asn Lys Glu
71      130                 135                 140
73  aac gat gct ttt aaa gaa agc gtt gat gaa agc gta gtt ggg gct ata         480
74  Asn Asp Ala Phe Lys Glu Ser Val Asp Glu Ser Val Val Gly Ala Ile
75  145                 150                 155                 160
77  ttt tta aac gct ctg tct aaa tat gaa gta gga aac cct tac aaa aag         528
78  Phe Leu Asn Ala Leu Ser Lys Tyr Glu Val Gly Asn Pro Tyr Lys Lys
79              165                 170                 175
81  aat tta aac cat aac aac cct ttc aaa cta ttg ctc tcg ctt tta aaa         576
82  Asn Leu Asn His Asn Asn Pro Phe Lys Leu Leu Leu Ser Leu Leu Lys
83              180                 185                 190
85  cga ctc aaa aat gcc cat cta acc ccc cta tct gtc aaa gaa atc cct         624
86  Arg Leu Lys Asn Ala His Leu Thr Pro Leu Ser Val Lys Glu Ile Pro
87              195                 200                 205
89  att tta ctt tgt tgg aaa gac gat aac gct aat ggg ctt tat gac tac         672
90  Ile Leu Leu Cys Trp Lys Asp Asp Asn Ala Asn Gly Leu Tyr Asp Tyr
91      210                 215                 220
93  att att cgt tta aga caa gaa atc gtt act atc aat aaa aca gaa ttc         720
94  Ile Ile Arg Leu Arg Gln Glu Ile Val Thr Ile Asn Lys Thr Glu Phe
95  225                 230                 235                 240
97  agc tac tca gat gaa ttt atc tat gaa aaa tgc cta aaa ctt tta gaa         768
98  Ser Tyr Ser Asp Glu Phe Ile Tyr Glu Lys Cys Leu Lys Leu Leu Glu
99              245                 250                 255
101 agt gtt aat aaa aca cga ttt aaa atg agc caa atc act aac gaa gcc         816
102 Ser Val Asn Lys Thr Arg Phe Lys Met Ser Gln Ile Thr Asn Glu Ala
103             260                 265                 270
105 gtt gat gaa tac att aga aaa atg cgt att aca gga ctt att tca ttg         864
106 Val Asp Glu Tyr Ile Arg Lys Met Arg Ile Thr Gly Leu Ile Ser Leu
107             275                 280                 285
109 cgt ggt aat ggt agg ttt att gat att aat act aat gaa aat aat aaa         912
110 Arg Gly Asn Gly Arg Phe Ile Asp Ile Asn Thr Asn Glu Asn Asn Lys
111     290                 295                 300
113 ata gat tac att tta caa acc cat aag gct ttt aaa ggg gat tat tta         960
114 Ile Asp Tyr Ile Leu Gln Thr His Lys Ala Phe Lys Gly Asp Tyr Leu
115 305                 310                 315                 320
117 aac gac act caa gct aac aaa ctc gcc ttt ttt aac tac atg gcg atc        1008
118 Asn Asp Thr Gln Ala Asn Lys Leu Ala Phe Phe Asn Tyr Met Ala Ile
119             325                 330                 335
121 gtg gat agc ttt ctt gtt agt gtt act cca atc agc gct aat gag agc        1056
122 Val Asp Ser Phe Leu Val Ser Val Thr Pro Ile Ser Ala Asn Glu Ser
123             340                 345                 350
125 gtt aaa tca agc aaa ttg aat gaa cta gca aac act tat act aaa gat        1104
126 Val Lys Ser Ser Lys Leu Asn Glu Leu Ala Asn Thr Tyr Thr Lys Asp
127             355                 360                 365
129 ttt atc aag caa gaa tta ctc att act tgt aac aag caa gaa tca aaa        1152
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133 gat agt ttt tta aga ctc att gat aaa cct tta cgc tta gaa ttt tta      1200
134 Asp Ser Phe Leu Arg Leu Ile Asp Lys Pro Leu Arg Leu Glu Phe Leu
135 385             390             395             400
137 agc gct att ttc ttg aaa caa cat ttt gaa aat tta agc gtg ata ccc      1248
138 Ser Ala Ile Phe Leu Lys Gln His Phe Glu Asn Leu Ser Val Ile Pro
139             405             410             415
141 aat tat aaa agc gat gat gaa ggc ttg ccc gta tac aca gca agc ggt      1296
142 Asn Tyr Lys Ser Asp Asp Glu Gly Leu Pro Val Tyr Thr Ala Ser Gly
143             420             425             430
145 aat aaa cct gat att gta gct atg gac aca aaa gcc caa agt tat ata      1344
146 Asn Lys Pro Asp Ile Val Ala Met Asp Thr Lys Ala Gln Ser Tyr Ile
147             435             440             445
149 gaa gtg agc ttg att aga gac aga agt caa agt acc ttg gaa atg ata      1392
150 Glu Val Ser Leu Ile Arg Asp Arg Ser Gln Ser Thr Leu Glu Met Ile
151     450             455             460
153 cct att gcc aga cat tta aaa gaa ttg att aaa aat agc acc gat att      1440
154 Pro Ile Ala Arg His Leu Lys Glu Leu Ile Lys Asn Ser Thr Asp Ile
155 465             470             475             480
157 aga gaa aaa ttt agt gtt ttt gta gct cca aat atc cat gat gat gcc      1488
158 Arg Glu Lys Phe Ser Val Phe Val Ala Pro Asn Ile His Asp Asp Ala
159             485             490             495
161 aaa gaa tat gcg gaa ttt gcc caa ttc aaa gac aat att aat ata tgt      1536
162 Lys Glu Tyr Ala Glu Phe Ala Gln Phe Lys Asp Asn Ile Asn Ile Cys
163             500             505             510
165 tgt tat gct att aat gat ttt atc aaa aaa gta gaa aac agc ata gaa      1584
166 Cys Tyr Ala Ile Asn Asp Phe Ile Lys Lys Val Glu Asn Ser Ile Glu
167             515             520             525
169 tgg tta cag atc aat gac cat ttg aaa gct taa                          1617
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171     530             535
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175 <211> LENGTH: 538
176 <212> TYPE: PRT
177 <213> ORGANISM: Helicobacter pylori
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186             20              25              30
189 Glu Asn Gln Ile Leu Lys Ser Ser Ile Ile Met Gln Ile Ile Lys Ser
190             35              40              45
193 Val Leu Ala His Arg Leu Tyr Arg Pro Thr Ser Leu Asn Gln Asn Lys
194     50              55              60
197 Glu Leu Lys Glu Lys Phe Asp Ser Asn Glu Tyr Val Phe Ser Asp Glu
198 65              70              75              80
201 Glu Leu Glu Arg Ile Ile Glu Ile Ser Pro Gln Asn His Lys Glu Met
202             85              90              95
```

```
205 Gly Phe Glu His Gly Trp Glu Ser Arg Phe Asp Thr Trp Tyr Lys Leu
206             100                 105             110
209 Met Cys Glu Phe Gly Phe Cys Tyr Tyr Ala Lys Tyr Glu Lys Ile Leu
210         115             120             125
213 Ile Ser Asp Ser Ala Lys Met Leu Ile Leu Ala Tyr Tyr Asn Lys Glu
214     130             135             140
217 Asn Asp Ala Phe Lys Glu Ser Val Asp Glu Ser Val Val Gly Ala Ile
218 145             150             155             160
221 Phe Leu Asn Ala Leu Ser Lys Tyr Glu Val Gly Asn Pro Tyr Lys Lys
222             165             170             175
225 Asn Leu Asn His Asn Asn Pro Phe Lys Leu Leu Leu Ser Leu Leu Lys
226             180             185             190
229 Arg Leu Lys Asn Ala His Leu Thr Pro Leu Ser Val Lys Glu Ile Pro
230         195             200             205
233 Ile Leu Leu Cys Trp Lys Asp Asp Asn Ala Asn Gly Leu Tyr Asp Tyr
234     210             215             220
237 Ile Ile Arg Leu Arg Gln Glu Ile Val Thr Ile Asn Lys Thr Glu Phe
238 225             230             235             240
241 Ser Tyr Ser Asp Glu Phe Ile Tyr Glu Lys Cys Leu Lys Leu Leu Glu
242             245             250             255
245 Ser Val Asn Lys Thr Arg Phe Lys Met Ser Gln Ile Thr Asn Glu Ala
246             260             265             270
249 Val Asp Glu Tyr Ile Arg Lys Met Arg Ile Thr Gly Leu Ile Ser Leu
250         275             280             285
253 Arg Gly Asn Gly Arg Phe Ile Asp Ile Asn Thr Asn Glu Asn Asn Lys
254     290             295             300
257 Ile Asp Tyr Ile Leu Gln Thr His Lys Ala Phe Lys Gly Asp Tyr Leu
258 305             310             315             320
261 Asn Asp Thr Gln Ala Asn Lys Leu Ala Phe Phe Asn Tyr Met Ala Ile
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265 Val Asp Ser Phe Leu Val Ser Val Thr Pro Ile Ser Ala Asn Glu Ser
266             340             345             350
269 Val Lys Ser Ser Lys Leu Asn Glu Leu Ala Asn Thr Tyr Thr Lys Asp
270             355             360             365
273 Phe Ile Lys Gln Glu Leu Leu Ile Thr Cys Asn Lys Gln Glu Ser Lys
274     370             375             380
277 Asp Ser Phe Leu Arg Leu Ile Asp Lys Pro Leu Arg Leu Glu Phe Leu
278 385             390             395             400
281 Ser Ala Ile Phe Leu Lys Gln His Phe Glu Asn Leu Ser Val Ile Pro
282             405             410             415
285 Asn Tyr Lys Ser Asp Asp Glu Gly Leu Pro Val Tyr Thr Ala Ser Gly
286             420             425             430
289 Asn Lys Pro Asp Ile Val Ala Met Asp Thr Lys Ala Gln Ser Tyr Ile
290         435             440             445
293 Glu Val Ser Leu Ile Arg Asp Arg Ser Gln Ser Thr Leu Glu Met Ile
294     450             455             460
297 Pro Ile Ala Arg His Leu Lys Glu Leu Ile Lys Asn Ser Thr Asp Ile
298 465             470             475             480
301 Arg Glu Lys Phe Ser Val Phe Val Ala Pro Asn Ile His Asp Asp Ala
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302                 485               490               495
305 Lys Glu Tyr Ala Glu Phe Ala Gln Phe Lys Asp Asn Ile Asn Ile Cys
306             500               505               510
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310       515               520               525
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314     530               535
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320 <213> ORGANISM: Helicobacter pylori
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324 <221> NAME/KEY: CDS
325 <222> LOCATION: (1)..(780)
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330 1               5                   10                  15
332 ttt aat caa gct tta aag cta gaa gaa aat tat ttt agc caa cat ttt       96
333 Phe Asn Gln Ala Leu Lys Leu Glu Glu Asn Tyr Phe Ser Gln His Phe
334             20                  25                  30
336 agc aac aag ttt ttc agc tat aaa gat tgt gtc aaa atc ggt agc att      144
337 Ser Asn Lys Phe Phe Ser Tyr Lys Asp Cys Val Lys Ile Gly Ser Ile
338             35                  40                  45
340 aga gag cat ata gaa agc tta aac tta gat aaa tta aat aaa gat att      192
341 Arg Glu His Ile Glu Ser Leu Asn Leu Asp Lys Leu Asn Lys Asp Ile
342     50                  55                  60
344 tta tta aca agc ctg att tat tca atg gat aag ata gct aac acg gta      240
345 Leu Leu Thr Ser Leu Ile Tyr Ser Met Asp Lys Ile Ala Asn Thr Val
346 65                  70                  75                  80
348 ggg cat tat gaa gct tat agg aaa aaa gag att ttg caa gat aga ttt      288
349 Gly His Tyr Glu Ala Tyr Arg Lys Lys Glu Ile Leu Gln Asp Arg Phe
350             85                  90                  95
352 att ttt gag ctt att agc cct ata aaa cat gat aaa aat atc atg ata      336
353 Ile Phe Glu Leu Ile Ser Pro Ile Lys His Asp Lys Asn Ile Met Ile
354             100                 105                 110
356 gag aga aaa aac gct aac gaa ttg gct aaa acc tta aaa ata gac tta      384
357 Glu Arg Lys Asn Ala Asn Glu Leu Ala Lys Thr Leu Lys Ile Asp Leu
358             115                 120                 125
360 gtc ttt att gat cct cca tac aat tca agg caa tac agc cgg ttt tat      432
361 Val Phe Ile Asp Pro Pro Tyr Asn Ser Arg Gln Tyr Ser Arg Phe Tyr
362     130                 135                 140
364 cat ctc tat gaa aac cta gtg cag tgg aaa aaa ccc aaa ctc tat gga      480
365 His Leu Tyr Glu Asn Leu Val Gln Trp Lys Lys Pro Lys Leu Tyr Gly
366 145                 150                 155                 160
368 aca gct tta aag cca tca tgc gag aac atg agc gaa tat tgc cgc tct      528
369 Thr Ala Leu Lys Pro Ser Cys Glu Asn Met Ser Glu Tyr Cys Arg Ser
370             165                 170                 175
372 aat gcc aag aaa gaa ttg agc gat tta att gaa aaa cta gat tgt aaa      576
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VERIFICATION SUMMARY   DATE: 07/30/2004
PATENT APPLICATION: **US/10/796,669A**   TIME: 11:26:56

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